

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2010; month=12; day=1; hr=14; min=55; sec=30; ms=225;]

=====

Application No: 10576440 Version No: 2.0

Input Set:

Output Set:

Started: 2010-11-26 11:59:33.492
Finished: 2010-11-26 11:59:33.594
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 102 ms
Total Warnings: 0
Total Errors: 0
No. of SeqIDs Defined: 2
Actual SeqID Count: 2

SEQUENCE LISTING

<110> BOUREL, DOMINIQUE
GLACET, ARNAUD
JORIEUX, SYLVIE
STURA, ENRICO
DUCANCEL, FREDERIC
TEILLAUD, JEAN-LUC

<120> USE OF METALLIC CATIONS TO IMPROVE FUNCTIONAL ACTIVITY OF
ANTIBODIES

<130> 096183-0104

<140> 10576440

<141> 2010-11-26

<150> PCT/FR2004/002687

<151> 2004-10-20

<150> FR 0312228

<151> 2003-10-20

<160> 2

<170> PatentIn version 3.5

<210> 1

<211> 1428

<212> DNA

<213> Homo sapiens

<220>

<223> cDNA sequence of double mutant His310-435Lys

<400> 1

atggagtttg ggctgagctg ggttttcctc gttgctcttt taagaggtgt ccagtgtcag	60
gtgcagctgg tggagtctgg gggaggcgtg gtccagcctg ggaggtccct gagactctcc	120
tgtacagcct ctggattcac cttcaaaaac tatgctatgc attgggtccg ccaggctcca	180
gccaaggggc tggagtgggt ggcaactata tcatatgatg gaaggaatat acaatatgca	240
gactccgtga agggccgatg caccttctcc agagacaatt ctcaggacac cctgtatctg	300
caactgaaca gcctcagacc ggaggacacg gctgtgtatt actgtgcgag acccgtaaga	360
agccgatggc tgcaattagg tcttgaagat gcttttcata tctggggcca ggggacaatg	420
gtcacctgtc cttcagctc caccaagggc ccacgggtct tccccctggc accctcctcc	480
aagagcacct ctgggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa	540
cgggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttccccggt	600

gtcctacagt cctcaggact ctactccctc agcagcgtgg tgaccgtgcc ctccagcagc 660

ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac 720

aagaaagttg agcccaaadc ttgtgacaaa actcacacat gcccacctgt cccagcacct 780

gaactcctgg ggggaccgtc agtcttcttc ttccccccaa aaccaagga caccctcatg 840

atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag 900

gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 960

gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gaagcaggac 1020

tggctgaatg gcaaggagta caagtgcaag gtctccaaca aagccctccc agcccccatc 1080

gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc 1140

ccatcccggt atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc 1200

tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag 1260

accacgcctc cctgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 1320

gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1380

cacaacaagt acacgcagaa gagcctctcc ctgtctccgg gtaaatag 1428

<210> 2

<211> 475

<212> PRT

<213> Homo sapiens

<220>

<223> Peptide sequence of double mutant His310-H435Lys.

<400> 2

Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Leu Arg Gly
1 5 10 15

Val Gln Cys Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln
20 25 30

Pro Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe
35 40 45

Lys Asn Tyr Ala Met His Trp Val Arg Gln Ala Pro Ala Lys Gly Leu
50 55 60

Glu Trp Val Ala Thr Ile Ser Tyr Asp Gly Arg Asn Ile Gln Tyr Ala
65 70 75 80

Asp	Ser	Val	Lys	Gly	Arg	Cys	Thr	Phe	Ser	Arg	Asp	Asn	Ser	Gln	Asp	85	90	95
Thr	Leu	Tyr	Leu	Gln	Leu	Asn	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	100	105	110
Tyr	Tyr	Cys	Ala	Arg	Pro	Val	Arg	Ser	Arg	Trp	Leu	Gln	Leu	Gly	Leu	115	120	125
Glu	Asp	Ala	Phe	His	Ile	Trp	Gly	Gln	Gly	Thr	Met	Val	Thr	Val	Ser	130	135	140
Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	145	150	155
Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	165	170	175
Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	180	185	190
Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	195	200	205
Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	210	215	220
Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	225	230	235
Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	245	250	255
Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	260	265	270
Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	275	280	285
Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	290	295	300

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
305 310 315 320

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
325 330 335

Leu Lys Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
340 345 350

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
355 360 365

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
370 375 380

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
385 390 395 400

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
405 410 415

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
420 425 430

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
435 440 445

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Lys Tyr
450 455 460

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475